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RAW SEQUENCE LISTING DATE: 08/23/2001
PATENT APPLICATION: **US/09/749,637A** TIME: 12:16:51

Input Set : **A:\227a-rsq.txt**
Output Set: **N:\CRF3\08162001\I749637A.raw**

<110> APPLICANT: University of Utah Research Foundation
Cognetix, Inc.
Olivera, Baldomero M.
Cartier, G. Edward
Watkins, Maren
Hillyard, David R.
McIntosh, J. Michael
Layer, Richard T.
Jones, Robert M.
<120> TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
<130> FILE REFERENCE: 2314-227
<140> CURRENT APPLICATION NUMBER: US 09/749,637A
<141> CURRENT FILING DATE: 2000-12-28
<150> PRIOR APPLICATION NUMBER: US 60/243,412
<151> PRIOR FILING DATE: 2000-10-27
<150> PRIOR APPLICATION NUMBER: US60/219,440
<151> PRIOR FILING DATE: 2000-07-20
<150> PRIOR APPLICATION NUMBER: US 60/214,263
<151> PRIOR FILING DATE: 2000-06-26
<150> PRIOR APPLICATION NUMBER: US 60/173,754
<151> PRIOR FILING DATE: 1999-12-30
<160> NUMBER OF SEQ ID NOS: 409
<170> SOFTWARE: PatentIn version 3.0
<210> SEQ ID NO: 1
<211> LENGTH: 261
<212> TYPE: DNA
<213> ORGANISM: Conus gloriamaris
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(231)
<400> SEQUENCE: 1

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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag att ctt       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
            20                  25                  30

ttt ccg aag gcg ggt cac gaa atg gag aac ctc gaa gtc tct aat cgg      144
Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
        35                  40                  45

gtc aag ccg tgc cgt aaa gaa ggt caa ctt tgt gat ccg ata ttt caa      192
Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
    50                  55                  60

aac tgc tgc cgt ggc tgg aat tgc gtt ctt ttc tgc gtc tgaaactacc      241
Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
65                  70                  75

gtgatgtctt ctctcccctc                                              261
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Input Set : A:\227a-rsq.txt
Output Set: N:\CRF3\08162001\I749637A.raw

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     70 <212> TYPE: PRT
     71 <213> ORGANISM: Conus gloriamaris
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     74 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
     75 1               5                  10                  15
     77 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
     78             20                  25                  30
     80 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
     81         35                  40                  45
     83 Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
     84     50                  55                  60
     86 Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
     87 65                  70                  75
     89 <210> SEQ ID NO: 3
     90 <211> LENGTH: 29
     91 <212> TYPE: PRT
     92 <213> ORGANISM: Conus gloriamaris
     94 <220> FEATURE:
     95 <221> NAME/KEY: SITE
     96 <222> LOCATION: (1)..(29)
     97 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at
residu
     98       e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp
     99       or bromo-Trp
    101 <400> SEQUENCE: 3
W--> 102 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
    103 1               5                  10                  15
W--> 105 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
    106             20                  25
    108 <210> SEQ ID NO: 4
    109 <211> LENGTH: 29
    110 <212> TYPE: PRT
    111 <213> ORGANISM: Conus gloriamaris
    113 <220> FEATURE:
    114 <221> NAME/KEY: SITE
    115 <222> LOCATION: (1)..(29)
    116 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at
residu
    117       e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 15 may be Tyr
    118       , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospn
    119       o-Tyr; Xaa at residue 22 may be Trp or bromo-Trp
    121 <400> SEQUENCE: 4
W--> 122 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Xaa Gln
    123 1               5                  10                  15
W--> 125 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
    126             20                  25
    128 <210> SEQ ID NO: 5
    129 <211> LENGTH: 29
    130 <212> TYPE: PRT
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Input Set : A:\227a-rsq.txt
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     131 <213> ORGANISM: Conus gloriamaris
     133 <220> FEATURE:
     134 <221> NAME/KEY: SITE
     135 <222> LOCATION: (1)..(29)
     136 <223> OTHER INFORMATION: Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at
residu
     137       e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp
     138       or bromo-Trp; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo
     139       -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospno-Tyr
     141 <400> SEQUENCE: 5
W--> 142 Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
     143 1               5                   10                  15
W--> 145 Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Xaa Cys Val
     146             20                  25
     148 <210> SEQ ID NO: 6
     149 <211> LENGTH: 542
     150 <212> TYPE: DNA
     151 <213> ORGANISM: Conus omaria
     153 <220> FEATURE:
     154 <221> NAME/KEY: CDS
     155 <222> LOCATION: (146)..(235)
     157 <400> SEQUENCE: 6
     158 gaagctggta cgcctgcagg taccggtccg gaattcccgg gtcgacatca tcatcatcga     60
     160 tccatctgtc catccatcca ttcattcatt cgctgccaga ctataataaa cattcaagtc    120
     162 tctctttctt tttgtgtctg acaga tcg atc agg atg tgc cgt aga gaa gct      172
     163                           Ser Ile Arg Met Cys Arg Arg Glu Ala
     164                           1               5
     166 caa ctt tgt gat ccg att ttt caa aac tgc tgc cat ggc ttg ttt tgc      220
     167 Gln Leu Cys Asp Pro Ile Phe Gln Asn Cys Cys His Gly Leu Phe Cys
     168 10                  15                  20                  25
     170 gtt ttg gtc tgc gtc taaaactacc gtgatgtctt ctcctcccct ctagtagtag      275
     171 Val Leu Val Cys Val
     172                 30
     174 taggcggccg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt    335
     176 ctatagtgtc acctaaattc aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa    395
     178 accctggcgt tacccaactt aatcgccttg cagcacatcc ccctttcgcc agctggcgta    455
     180 atagcgaaga ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg aatggcgaat    515
     182 gggacgcgcc ctgtagcggc gcattat                                       542
     184 <210> SEQ ID NO: 7
     185 <211> LENGTH: 30
     186 <212> TYPE: PRT
     187 <213> ORGANISM: Conus omaria
     189 <400> SEQUENCE: 7
     190 Ser Ile Arg Met Cys Arg Arg Glu Ala Gln Leu Cys Asp Pro Ile Phe
     191 1               5                   10                  15
     193 Gln Asn Cys Cys His Gly Leu Phe Cys Val Leu Val Cys Val
     194             20                  25                  30
     196 <210> SEQ ID NO: 8
     197 <211> LENGTH: 27
     198 <212> TYPE: PRT
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Input Set : A:\227a-rsq.txt
Output Set: N:\CRF3\08162001\I749637A.raw

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     199 <213> ORGANISM: Conus omaria
     201 <220> FEATURE:
     202 <221> NAME/KEY: SITE
     203 <222> LOCATION: (1)..(27)
     204 <223> OTHER INFORMATION: Xaa at residue 5 is Glu or gamma-carboxy-Glu; Xaa at residue
11 m
     205       ay be Pro or hydroxy-Pro
     207 <400> SEQUENCE: 8
W--> 208 Met Cys Arg Arg Xaa Ala Gln Leu Cys Asp Xaa Ile Phe Gln Asn Cys
     209 1               5                   10                  15
     211 Cys His Gly Leu Phe Cys Val Leu Val Cys Val
     212             20                  25
     214 <210> SEQ ID NO: 9
     215 <211> LENGTH: 346
     216 <212> TYPE: DNA
     217 <213> ORGANISM: Conus textile
     219 <220> FEATURE:
     220 <221> NAME/KEY: CDS
     221 <222> LOCATION: (25)..(315)
     223 <400> SEQUENCE: 9
     224 ggcattacct aaaacatcac caag atg aaa ctg acg tgc atg atg atc gtt        51
     225                           Met Lys Leu Thr Cys Met Met Ile Val
     226                           1               5
     228 gct gtg ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gat gac tcc        99
     229 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser
     230 10                  15                  20                  25
     232 aga aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag      147
     233 Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu
     234                 30                  35                  40
     236 aac ctc gaa gac tct aaa cac agg cac cag gag aga ccg gac acc ggc      195
     237 Asn Leu Glu Asp Ser Lys His Arg His Gln Glu Arg Pro Asp Thr Gly
     238             45                  50                  55
     240 gac aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa      243
     241 Asp Lys Glu Glu Met Leu Leu Gln Arg Gln Val Lys Pro Cys Arg Lys
     242         60                  65                  70
     244 gaa cat caa ctt tgt gat ctg att ttt caa aac tgc tgc cgt ggc tgg      291
     245 Glu His Gln Leu Cys Asp Leu Ile Phe Gln Asn Cys Cys Arg Gly Trp
     246     75                  80                  85
     248 tat tgc gtt gtt ctg tct tgc act tgaaagctac ctgatgtgtt ctactcccat     345
     249 Tyr Cys Val Val Leu Ser Cys Thr
     250 90                  95
     252 c                                                               346
     254 <210> SEQ ID NO: 10
     255 <211> LENGTH: 97
     256 <212> TYPE: PRT
     257 <213> ORGANISM: Conus textile
     259 <400> SEQUENCE: 10
     260 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
     261 1               5                   10                  15
     263 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Met Glu Asn Leu
```

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Input Set : **A:\227a-rsq.txt**
Output Set: **N:\CRF3\08162001\I749637A.raw**

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     264             20                  25                  30
     266 Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Asp Ser Lys His
     267         35                  40                  45
     269 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
     270     50                  55                  60
     272 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
     273 65                  70                  75                  80
     275 Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Val Val Leu Ser Cys
     276                 85                  90                  95
     278 Thr
     280 <210> SEQ ID NO: 11
     281 <211> LENGTH: 31
     282 <212> TYPE: PRT
     283 <213> ORGANISM: Conus textile
     285 <220> FEATURE:
     286 <221> NAME/KEY: SITE
     287 <222> LOCATION: (1)..(31)
     288 <223> OTHER INFORMATION: Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residue 4
may be
     289       Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-carboxy-
     290       Glu; Xaa at residue 23 may be Trp or bromo-Trp; Xaa at residue 24
     292 <220> FEATURE:
     293 <221> NAME/KEY: SITE
     294 <222> LOCATION: (1)..(31)
     295 <223> OTHER INFORMATION: may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-
Tyr
     296       or O-phospho-Tyr
     298 <400> SEQUENCE: 11
W--> 299 Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Phe
     300 1               5                   10                  15
W--> 302 Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Val Val Leu Ser Cys Thr
     303             20                  25                  30
     305 <210> SEQ ID NO: 12
     306 <211> LENGTH: 265
     307 <212> TYPE: DNA
     308 <213> ORGANISM: Conus omaria
     310 <220> FEATURE:
     311 <221> NAME/KEY: CDS
     312 <222> LOCATION: (1)..(234)
     314 <400> SEQUENCE: 12
     315 atg aaa ctg acg tgc ctg atg atc gtt gcc gtg ctg tcc ttg acc ggc       48
     316 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Ser Leu Thr Gly
     317 1               5                   10                  15
     319 tgg aca ttc gtc acg gct gat gac tct gga aat gga ttg ggg aat ctt       96
     320 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu
     321             20                  25                  30
     323 ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg      144
     324 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
     325         35                  40                  45
     327 aac aag agg tgc gtt cca cac gag ggc cct tgt aat tgg ctt aca caa      192
     328 Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln
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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 08/23/2001
PATENT APPLICATION: US/09/749,637A TIME: 12:16:52

Input Set : A:\227a-rsq.txt
Output Set: N:\CRF3\08162001\I749637A.raw

L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:876 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:951 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:1327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:1342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:1361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:1574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:1648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66

VERIFICATION SUMMARY DATE: 08/23/2001
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Input Set : **A:\227a-rsq.txt**
Output Set: **N:\CRF3\08162001\I749637A.raw**

L:1718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69